

WE CLAIM THE FOLLOWING:

1. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising nine α -carbons having interatomic distances in Angstroms between said α -carbons
- 5 that are ± 2.3 Angstroms of the following interatomic distances:

α -Carbon	1	2	3	4	5	6	7	8	9
1	0.0	8.4	13.7	12.7	11.9	10.2	13.1	9.4	12.8
2	8.4	0.0	11.3	8.7	10.2	7.2	14.8	15.1	17.4
3	13.7	11.3	0.0	3.8	5.4	9.3	6.6	13.9	13.7
4	12.7	8.7	3.8	0.0	3.8	6.0	9.2	15.4	16.1
5	11.9	10.2	5.4	3.8	0.0	5.0	7.8	14.6	15.5
6	10.2	7.2	9.3	6.0	5.0	0.0	12.0	16.1	18.0
7	13.1	14.8	6.6	9.2	7.8	12.0	0.0	10.2	9.5
8	9.4	15.1	13.9	15.4	14.6	16.1	10.2	0.0	3.8
9	12.8	17.4	13.7	16.1	15.5	18.0	9.5	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	120.203	38.695	43.506
2	114.058	43.884	41.015
3	106.807	36.336	45.151
4	107.629	38.010	41.804
5	109.375	34.842	40.617
6	111.944	37.854	37.602
7	110.233	31.098	47.361
8	118.846	34.443	51.796
9	116.461	32.848	54.290

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, each said α -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 9

Ordered Arrangements of α -Carbons 1-9									
	1	2	3	4	5	6	7	8	9
A	W	I	T	T	Y	L	C	T	Y
B	W	I	S	T	Y	L	C	T	Y
C	W	I	C	G	Y	L	C	L	Y
D	W	I	S	G	Y	L	C	L	Y
E	W	L	A	G	Y	I	A	L	Y
F	W	L	T	V	H	L	G	V	Y
G	W	L	A	G	Y	I	A	L	Y
H	W	I	V	G	N	L	F	L	Y
I	W	I	T	A	G	L	S	C	Y
J	W	V	S	C	I	M	G	S	Y
K	W	F	I	T	A	T	G	T	Y
L	W	N	I	S	G	M	L	M	Y
M	W	V	S	S	Y	L	G	L	Y
N	W	F	T	L	A	L	G	S	Y
O	W	N	S	G	P	L	L	M	Y
P	W	N	G	I	L	L	L	I	Y
Q	Y	L	V	T	M	T	G	T	Y
R	W	I	I	S	A	I	L	I	Y
S	W	F	S	S	V	I	L	I	Y
T	W	I	V	A	S	I	L	I	Y
U	W	N	I	S	S	I	F	M	Y
V	L	A	I	G	Q	L	S	I	F
W	S	I	A	L	V	S	L	G	Y
X	L	C	C	G	H	I	L	V	Y
Y	S	C	S	S	V	I	L	G	Y
Z	W	A	S	G	M	L	G	I	Y

Table 9

AA	A	N	L	T	S	T	C	L	Y
BB	L	C	S	A	Y	V	L	L	Y
CC	W	A	T	G	M	L	S	M	Y
DD	M	C	S	S	G	I	L	V	Y
EE	S	G	V	G	L	C	W	F	Y
FF	S	G	A	L	G	V	G	F	Y
GG	S	G	F	A	L	I	G	F	Y
HH	A	G	V	T	G	L	I	G	Y
II	W	V	T	G	L	V	I	S	Y
JJ	W	A	S	G	M	L	G	I	Y
KK	W	I	S	T	Y	L	C	T	Y
LL	W	I	T	T	Y	L	C	T	Y
MM	W	N	I	S	G	M	L	M	F
NN	A	A	I	G	Q	L	S	I	Y
OO	A	I	V	A	S	I	L	I	Y

2. The synthase of claim 1, wherein said synthase has 25% or greater sequence identity to residues 265 to 535 of SEQ ID 2.
3. The synthase of claim 2, wherein said synthase has 35% or greater sequence identity to residues 265 to 535 of SEQ ID 2.
4. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.
5. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.
6. The synthase of claim 1, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.
7. The synthase of claims 4, 5, or 6, wherein said product is a cyclic terpenoid hydrocarbon.
8. The synthase of claim 4, 5, or 6, wherein said product is an acyclic terpenoid hydrocarbon.
9. The synthase of claim 4, 5, or 6 wherein said product is a cyclic hydroxylated terpenoid hydrocarbon.
10. The synthase of claim 4, 5, or 6 wherein said product is an acyclic hydroxylated terpenoid hydrocarbon.
11. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Cys, Ser, and Thr.
12. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Phe, Tyr and Trp.

13. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Pro, Gly, and Ala.
14. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Glu and Asp.
15. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Met, Ile, Val and Leu.
- 10 16. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Arg and Lys.
17. The synthase of claim 1, wherein said R-group associated with said α -carbon 1 is selected from the group consisting of Gln, Asn and His.
- 15 18. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Cys, Ser and Thr.
19. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Phe, Tyr and Trp.
- 20 20. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Pro, Gly, and Ala.
21. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Glu and Asp.
- 25 22. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Met, Ile, Val and Leu.
- 30 23. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Arg and Lys.
24. The synthase of claim 1, wherein said R-group associated with said α -carbon 2 is selected from the group consisting of Gln, Asn and His.
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25. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Cys, Ser and Thr.

5 26. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Phe, Tyr and Trp.

27. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Pro, Gly, and Ala.

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28. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Glu and Asp.

15 29. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Met, Ile, Val and Leu.

30. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Arg and Lys.

20 31. The synthase of claim 1, wherein said R-group associated with said α -carbon 3 is selected from the group consisting of Gln, Asn and His.

32. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Cys, Ser and Thr.

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33. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Phe, Tyr and Trp.

30 34. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Pro, Gly, and Ala.

35. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Glu and Asp.

36. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Met, Ile, Val and Leu.

37. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Arg and Lys.

38. The synthase of claim 1, wherein said R-group associated with said α -carbon 4 is selected from the group consisting of Gln, Asn and His.

39. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Cys, Ser and Thr.

40. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Phe, Tyr and Trp.

41. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Pro, Gly, and Ala.

42. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Glu and Asp.

43. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Met, Ile, Val and Leu.

44. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Arg and Lys.

45. The synthase of claim 1, wherein said R-group associated with said α -carbon 5 is selected from the group consisting of Gln, Asn and His.

46. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Cys, Ser and Thr.

47. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Phe, Tyr and Trp.

48. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Pro, Gly, and Ala.
- 5 49. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Glu and Asp.
50. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Met, Ile, Val and Leu.
- 10 51. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Arg and Lys.
52. The synthase of claim 1, wherein said R-group associated with said α -carbon 6 is selected from the group consisting of Gln, Asn and His.
- 15 53. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Cys, Ser and Thr.
- 20 54. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Phe, Tyr and Trp.
55. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Pro, Gly, and Ala.
- 25 56. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Glu and Asp.
57. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Met, Ile, Val and Leu.
- 30 58. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Arg and Lys.

59. The synthase of claim 1, wherein said R-group associated with said α -carbon 7 is selected from the group consisting of Gln, Asn and His.
60. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Cys, Ser and Thr.
61. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Phe, Tyr and Trp.
62. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Pro, Gly, and Ala.
63. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Glu and Asp.
64. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Met, Ile, Val and Leu.
65. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Arg and Lys.
66. The synthase of claim 1, wherein said R-group associated with said α -carbon 8 is selected from the group consisting of Gln, Asn and His.
67. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Cys, Ser and Thr.
68. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Phe, Tyr and Trp.
69. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Pro, Gly, and Ala.
70. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Glu and Asp.

- 5 72. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Arg and Lys.

73. The synthase of claim 1, wherein said R-group associated with said α -carbon 9 is selected from the group consisting of Gln, Asn and His.

74. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said α -carbons 1 to 9 is Trp, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Phe, respectively.

- 15 75. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said α -carbons 1 to 9 is Ser, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Tyr, respectively.

76. The synthase of claim 1, wherein said ordered arrangement of R-
20 groups in said synthase associated with said α -carbons 1 to 9 is Trp, Ile, Thr, Thr,
Tyr, Leu, Trp, Thr and Tyr, respectively.

77. The synthase of claim 1, wherein said ordered arrangement of R-
groups in said synthase associated with said α -carbons 1 to 9 is Ser, Ile, Thr, Thr,
25 Tyr, Leu, Trp, Thr and Tyr, respectively.

78. The synthase of claim 1, wherein said ordered arrangement of R-groups in said synthase associated with said α -carbons 1 to 9 is Glu, Ile, Thr, Thr, Tyr, Leu, Cys, Thr and Tyr, respectively.

79. A terpene synthase made by aligning a primary amino acid sequence of a terpene synthase polypeptide to the amino acid sequence of residues 265 to 535 of SEQ ID NO: 2, mutating a nucleic acid encoding said polypeptide at one or more codons of nine amino acid residues in a region of said polypeptide having 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said nine residues

in said polypeptide aligning with residues 273, 294, 402, 403, 404, 407, 440, 519 and 520 of SEQ ID NO: 2; and expressing said mutated nucleic acid so that a mutated terpene synthase is made.

- 5 80. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising sixteen α -carbons, said α -carbons having interatomic distances in Angstroms between said α -carbons that are ± 2.3 Angstroms of the following interatomic distances:

00000000.062801

α -Carbon	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.0	5.0	6.0	10.5	9.0	14.3	13.0	13.5	11.2	15.6	12.5	11.8	15.0	13.7	8.3	11.0
2	5.0	0.0	8.4	13.3	12.4	13.7	12.7	11.9	10.2	13.1	9.2	9.4	12.8	13.6	9.3	12.9
3	6.0	8.4	0.0	5.3	6.0	11.3	8.7	10.2	7.2	14.8	13.9	15.1	17.4	15.7	11.3	13.3
4	10.5	13.3	5.3	0.0	3.8	10.7	8.3	11.4	9.6	16.1	16.8	18.1	19.6	16.8	13.3	13.9
5	9.0	12.4	6.0	3.8	0.0	10.8	9.6	12.5	11.6	15.5	15.4	15.9	17.3	13.8	10.1	10.3
6	14.3	13.7	11.3	10.7	10.8	0.0	3.8	5.4	9.3	6.6	10.5	13.9	13.7	12.9	12.8	14.1
7	13.0	12.7	8.7	8.3	9.6	3.8	0.0	3.8	6.0	9.2	12.1	15.4	16.1	15.3	13.8	15.4
8	13.5	11.9	10.2	11.4	12.5	5.4	3.8	0.0	5.0	7.8	10.5	14.6	15.5	16.0	14.7	17.0
9	11.2	10.2	7.2	9.6	11.6	9.3	6.0	5.0	0.0	12.0	12.8	16.1	18.0	18.2	15.3	17.8
10	15.6	13.1	14.8	16.1	15.5	6.6	9.2	7.8	12.0	0.0	5.9	10.2	9.5	11.4	12.8	14.9
11	12.5	9.2	13.9	16.8	15.4	10.5	12.1	10.5	12.8	5.9	0.0	5.0	6.0	9.5	9.7	12.8
12	11.8	9.4	15.1	18.1	15.9	13.9	15.4	14.6	16.1	12.2	5.0	0.0	3.8	7.1	7.2	10.2
13	15.0	12.8	17.4	19.6	17.3	13.7	16.1	15.5	18.0	9.5	6.0	3.8	0.0	5.8	8.3	10.8
14	13.7	13.6	15.7	16.8	13.8	12.9	15.3	16.0	18.2	11.4	9.5	7.1	5.8	0.0	5.7	5.7
15	8.3	9.3	11.3	13.3	10.1	12.8	13.8	14.7	15.3	12.8	9.7	7.2	8.8	5.7	0.0	3.8
16	11.0	12.9	13.3	13.9	10.3	14.1	15.4	17.0	17.8	14.9	12.8	10.2	10.8	5.7	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	119.144	43.487	44.133
2	120.203	38.695	43.506
3	114.058	43.884	41.015
4	109.327	46.145	41.743
5	110.682	46.410	45.284
6	106.807	36.336	45.151
7	107.629	38.010	41.804
8	109.375	34.842	40.617
9	111.944	37.854	37.602
10	110.233	31.098	47.361
11	115.915	32.218	48.369
12	118.846	34.443	51.796
13	116.461	32.848	54.290
14	114.100	38.006	55.620
15	116.617	41.285	51.702
16	114.855	43.486	54.238

, each said α -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 8

Ordered Arrangement of R-Groups at α -carbons 1-16																
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
A	C	W	I	I	S	T	T	Y	L	C	V	T	Y	D	Y	T
B	C	W	I	I	S	S	T	Y	L	C	I	T	Y	D	Y	T
C	G	W	I	A	S	C	G	Y	L	C	M	L	Y	D	Y	T
D	G	W	I	A	S	S	G	Y	L	C	M	L	Y	D	Y	T
E	C	W	L	T	S	A	G	Y	I	A	A	L	Y	D	Y	T
F	G	W	L	L	S	T	V	H	L	G	A	V	Y	D	Y	T
G	C	W	L	T	S	A	G	Y	I	A	A	L	Y	D	Y	T
H	L	W	I	T	T	V	G	N	L	F	V	L	Y	D	Y	T
I	P	W	I	V	D	T	A	G	L	S	A	C	Y	D	Y	T
J	A	W	V	C	G	S	C	I	M	G	C	S	Y	D	Y	T
K	N	F	F	L	G	I	T	A	T	G	I	T	Y	E	F	Q
L	C	W	N	I	T	I	S	G	M	L	A	M	Y	D	H	T
M	S	W	V	L	T	S	S	Y	L	G	V	L	Y	D	F	T
N	N	F	F	L	V	T	L	A	L	G	L	S	Y	E	F	T
O	C	W	N	I	T	S	G	P	L	L	A	M	Y	D	F	G
P	C	W	N	V	T	G	I	L	L	L	A	I	Y	D	F	G
Q	C	Y	L	L	T	V	T	M	T	G	I	T	Y	D	Y	T
R	C	W	I	I	T	I	S	A	I	L	A	I	Y	D	D	G
S	S	W	F	I	V	S	S	V	I	L	V	I	Y	D	H	G
T	S	W	I	A	T	V	A	S	I	L	A	I	Y	D	H	G
U	N	W	N	L	T	I	S	S	I	F	A	M	Y	D	H	G
V	F	L	A	Q	T	I	G	Q	L	S	T	I	F	D	F	G
W	I	S	C	T	V	I	A	L	V	G	M	F	Y	D	L	T
X	Y	L	S	I	T	C	G	H	S	L	F	G	Y	D	L	T
Y	G	S	F	I	T	S	S	V	I	L	A	V	Y	D	H	G
Z	Y	W	A	C	T	S	G	M	L	G	L	I	Y	D	L	Y

Table 8

AA	A	A	N	L	T	L	T	S	T	C	L	L	Y	D	Y	F	N
BB	F	L	C	V	T	S	A	Y	V	L	L	L	Y	D	Y	F	S
CC	F	W	A	M	T	T	G	M	L	S	I	M	Y	D	Y	F	S
DD	Y	M	C	V	T	S	S	G	I	L	F	V	Y	D	Y	Y	T
EE	V	S	G	Q	V	V	G	L	C	W	V	F	Y	D	Y	Y	G
FF	C	S	G	T	T	A	L	G	V	G	L	F	Y	D	Y	F	T
GG	C	S	G	T	T	F	A	L	I	G	L	F	Y	D	Y	F	T
HH	C	A	G	T	T	F	A	L	I	G	V	F	Y	D	Y	Y	T
II	I	W	V	I	S	T	G	L	V	I	T	S	Y	D	Y	L	Y
JJ	Y	W	A	C	T	S	G	M	L	G	L	I	Y	D	Y	Y	T
KK	C	W	I	I	S	S	T	Y	L	C	V	T	Y	D	Y	Y	T
LL	C	W	I	I	S	T	T	Y	L	C	I	T	Y	D	Y	Y	T
MM	C	W	N	I	T	I	S	G	M	L	A	M	Y	D	Y	H	G
NN	F	A	A	Q	T	I	G	Q	L	S	T	I	F	D	Y	F	G
OO	F	A	I	A	T	V	A	S	I	L	A	I	Y	D	Y	F	G

81. The synthase of claim 80, wherein said synthase has 25% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.

82. The synthase of claim 81, wherein said synthase has 35% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2.

83. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.

84. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.

85. The synthase of claim 81, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.

86. The synthase of claims 83, 84, or 85, wherein said product is a cyclic terpenoid hydrocarbon.

87. The synthase of claim 81, wherein said ordered arrangement of R-groups in said synthase associated with said α -carbons 1 to 16 is Cys, Trp, Ile, Ile, Ser, Thr, Thr, Tyr, Leu, Cys, Val, Thr, Tyr, Asp, Phe and Thr, respectively.

88. An isolated terpene synthase having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, said synthase comprising nineteen α -carbons having interatomic distances in Angstroms between said α -carbons that are ± 2.3 Angstroms of the following interatomic distances:

Table 2

α -carbon	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.0	5.0	6.0	10.5	9.0	19.8	16.8	14.3	13.0	13.5	11.2	15.6	16.7	12.5	11.8	15.0	13.7	8.3	11.0
2	5.0	0.0	8.4	13.3	12.4	21.3	16.8	13.7	12.7	11.9	10.2	13.1	15.4	9.2	9.4	12.8	13.6	9.3	12.9
3	8.0	8.4	0.0	5.3	6.0	15.3	12.6	11.3	8.7	10.2	7.2	14.8	16.8	13.9	15.1	17.4	15.7	11.3	13.3
4	10.5	13.3	5.3	0.0	3.8	11.0	10.4	10.7	8.3	11.4	9.6	16.1	17.0	16.8	18.1	19.6	16.8	13.3	13.9
5	9.0	12.4	6.0	3.8	0.0	11.8	11.1	10.8	9.8	12.5	11.6	15.5	15.2	15.4	15.9	17.3	13.8	10.1	10.3
6	19.8	21.3	15.3	11.0	11.8	0.0	8.4	9.9	10.2	13.6	15.5	16.2	15.8	20.0	22.2	21.8	18.7	16.5	18.0
7	16.8	16.8	12.8	10.4	11.1	6.4	0.0	3.8	5.0	7.8	11.0	10.1	11.1	14.3	17.4	17.0	15.3	15.3	15.9
8	14.3	13.7	11.3	10.7	10.8	9.9	3.8	0.0	3.8	5.4	9.3	8.8	8.6	10.5	13.9	13.7	12.9	12.8	14.1
9	13.0	12.7	8.7	8.3	9.8	10.2	5.0	3.8	0.0	3.8	6.0	9.2	12.1	12.1	15.4	16.1	15.3	13.8	15.4
10	13.5	11.9	10.2	11.4	12.5	13.6	7.8	5.4	3.8	0.0	5.0	7.8	12.4	10.5	14.6	15.5	16.0	14.7	17.0
11	11.2	10.2	7.2	9.6	11.8	15.5	11.0	9.3	6.0	5.0	0.0	12.0	16.2	12.8	16.1	18.0	18.2	15.3	17.8
12	15.6	13.1	14.8	16.1	15.5	18.2	10.1	6.6	9.2	7.8	12.0	0.0	6.0	5.9	10.2	9.5	11.4	12.8	14.9
13	16.7	15.4	16.8	17.0	15.2	15.8	11.1	8.6	12.1	12.4	16.2	8.0	0.0	8.2	9.8	7.4	7.3	11.0	11.7
14	12.5	9.2	13.9	16.8	15.4	20.0	14.3	10.5	12.1	10.5	12.8	5.9	8.2	0.0	5.0	6.0	9.5	9.7	12.8
15	11.8	9.4	15.1	18.1	15.9	22.2	17.4	13.9	15.4	14.8	16.1	10.2	9.8	5.0	0.0	3.8	7.1	7.2	10.2
16	15.0	12.8	17.4	19.8	17.3	21.8	17.0	13.7	16.1	15.5	18.0	9.5	7.4	6.0	3.8	0.0	5.8	8.8	10.8
17	13.7	13.8	15.7	16.8	13.8	18.7	15.3	12.9	15.3	16.0	18.2	11.4	7.3	9.5	7.1	5.8	0.0	5.7	5.7
18	8.3	9.3	11.3	13.3	10.1	18.5	15.3	12.8	13.8	14.7	15.3	12.8	11.0	9.7	7.2	8.8	5.7	0.0	3.8
19	11.0	12.9	13.3	13.9	10.3	18.0	15.9	14.1	15.4	17.0	17.8	14.9	11.7	12.8	10.2	10.8	5.7	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center points of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	119.144	43.487	44.133
2	120.203	38.695	43.506
3	114.058	43.884	41.015
4	109.327	46.145	41.743
5	110.682	46.410	45.284
6	99.381	42.920	45.148
7	103.445	38.054	44.605
8	106.807	36.336	45.151
9	107.629	38.010	41.804
10	109.375	34.842	40.617
11	111.944	37.854	37.602
12	110.233	31.098	47.361
13	109.178	33.314	52.875
14	115.915	32.218	48.369
15	118.846	34.443	51.796
16	116.461	32.848	54.290
17	114.100	38.006	55.620
18	116.617	41.285	51.702
19	114.855	43.486	54.238

, each said α -carbon having an associated R-group, said synthase having an ordered arrangement of said R-groups other than the following ordered arrangements of R-groups:

Table 7

Ordered Arrangement of R-Groups at α -carbons 1-19																			
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
A	C	W	I	I	S	Y	T	T	T	Y	L	C	D	V	T	Y	D	Y	T
B	C	W	I	I	S	Y	T	S	T	Y	L	C	D	I	T	Y	D	Y	T
C	G	W	I	A	S	Y	T	C	G	Y	L	C	D	M	L	Y	D	Y	T
D	G	W	I	A	S	Y	T	S	G	Y	L	C	D	M	L	Y	D	Y	T
E	C	W	L	T	S	Y	S	A	G	Y	I	A	N	A	L	Y	D	Y	T
F	G	W	L	L	S	Y	S	T	V	H	L	G	D	A	V	Y	D	Y	T
G	C	W	L	T	S	Y	S	A	G	Y	I	A	N	A	L	Y	D	Y	T
H	L	W	I	T	T	Y	S	V	G	N	L	F	D	V	L	Y	D	Y	T
I	P	W	I	V	D	Y	S	T	A	G	L	S	D	A	C	Y	D	Y	T
J	A	W	V	C	G	F	T	S	C	I	M	G	N	C	S	Y	D	Y	T
K	N	F	F	L	G	A	E	I	T	A	T	G	N	I	T	Y	D	Y	T
L	C	W	N	I	T	Y	S	I	S	G	M	L	D	A	M	Y	D	Y	T
M	S	W	V	L	T	Y	S	S	S	Y	L	G	G	V	L	Y	D	Y	T
N	N	F	V	L	V	N	A	T	L	A	L	G	N	L	S	Y	D	Y	T
O	C	W	N	I	T	Y	I	S	G	P	L	L	D	A	M	Y	D	Y	T
P	C	W	N	V	T	Y	I	G	G	I	L	L	D	A	I	Y	D	Y	T
Q	C	Y	L	L	T	F	A	V	T	M	T	G	N	I	T	Y	D	Y	T
R	C	W	I	I	T	Y	S	I	S	A	I	L	D	A	I	Y	D	Y	T
S	S	W	F	I	V	F	S	S	S	V	I	L	D	V	I	Y	D	Y	T
T	S	W	I	A	T	Y	S	S	V	A	S	I	L	A	I	Y	D	Y	T
U	N	W	N	L	T	Y	S	I	S	S	I	F	N	S	M	Y	D	Y	T
V	F	L	A	Q	T	Y	S	I	G	Q	L	S	D	T	I	F	D	Y	T
W	I	S	T	T	V	Y	S	I	A	L	V	G	N	M	F	Y	D	Y	T
X	Y	L	C	I	T	Y	S	C	G	H	S	L	G	F	G	Y	D	Y	T
Y	G	S	F	I	T	F	S	S	S	V	I	L	N	A	V	Y	D	Y	T
Z	Y	W	A	C	T	Y	S	S	G	M	L	G	D	L	I	Y	D	Y	T

Table 7

AA	A	A	N	L	T	N	A	L	T	S	T	C	M	L	L	Y	D	Y	N
BB	F	L	C	V	T	Y	S	S	A	Y	V	L	G	L	L	Y	D	F	S
CC	F	W	A	M	T	Y	N	T	G	M	L	S	D	I	L	Y	D	F	S
DD	Y	M	C	V	T	F	V	S	S	G	I	L	G	F	V	Y	D	Y	T
EE	V	S	G	Q	V	Y	S	V	G	L	C	W	N	V	F	Y	D	F	G
FF	C	S	G	T	T	M	F	A	L	G	V	G	N	L	F	Y	D	T	T
GG	C	S	G	T	T	M	S	F	A	L	I	G	N	L	F	Y	D	T	T
HH	C	A	G	T	T	M	S	F	A	L	I	G	N	L	F	Y	D	T	T
II	I	W	V	I	S	Y	T	T	G	L	V	I	N	T	S	Y	D	Y	T
JJ	Y	W	A	C	T	Y	S	T	G	M	L	G	D	L	I	Y	D	L	Y
KK	C	W	I	I	S	Y	T	S	T	Y	L	C	D	V	T	Y	D	Y	T
LL	C	W	I	I	S	Y	T	T	T	Y	L	C	D	I	T	Y	D	Y	T
MM	C	W	N	I	T	Y	S	I	S	G	M	L	D	A	M	Y	D	H	G
NN	F	A	A	Q	T	Y	S	I	G	Q	L	S	D	T	I	F	D	F	G
OO	F	A	I	A	T	Y	S	V	A	S	I	L	D	A	I	Y	D	F	G

09032011 09032011

91. The synthase of claim 88, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.

93. The synthase of claim 88, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.

94. The synthase of claims 91, 92, or 93; wherein said product is a cyclic terpenoid hydrocarbon.

a first domain having an amino terminal end and a carboxyl terminal end;
said first domain comprising amino acids that align structurally in three-dimensional space with a glycosyl hydrolase catalytic core, said glycosyl hydrolase catalytic core selected from the group consisting of amino acids 36 to 230 of glucoamylase PDB code 3GLY of *Aspergillus awamori* and amino acids 36 to 230 of endoglucanase CelD PDB code 1CLC;

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α -Carbon	1	2	3	4	5	6	7	8	9
1	0.0	8.4	13.7	12.7	11.9	10.2	13.1	9.4	12.8
2	8.4	0.0	11.3	8.7	10.2	7.2	14.8	15.1	17.4
3	13.7	11.3	0.0	3.8	5.4	9.3	6.6	13.9	13.7
4	12.7	8.7	3.8	0.0	3.8	6.0	9.2	15.4	16.1
5	11.9	10.2	5.4	3.8	0.0	5.0	7.8	14.6	15.5
6	10.2	7.2	9.3	6.0	5.0	0.0	12.0	16.1	18.0
7	13.1	14.8	6.6	9.2	7.8	12.0	0.0	10.2	9.5
8	9.4	15.1	13.9	15.4	14.6	16.1	10.2	0.0	3.8
9	12.8	17.4	13.7	16.1	15.5	18.0	9.5	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	120.203	38.695	43.506
2	114.058	43.884	41.015
3	106.807	36.336	45.151
4	107.629	38.010	41.804
5	109.375	34.842	40.617
6	111.944	37.854	37.602
7	110.233	31.098	47.361
8	118.846	34.443	51.796
9	116.461	32.848	54.290

, each said α -carbon having an associated R-group, said synthase having an ordered arrangement of R-groups other than the following ordered arrangements of R-groups:

Table 9

Ordered Arrangements of α -Carbons 1-9									
	1	2	3	4	5	6	7	8	9
A	W	I	T	T	Y	L	C	T	Y
B	W	I	S	T	Y	L	C	T	Y
C	W	I	S	G	Y	L	C	L	Y
D	W	I	S	G	Y	L	C	L	Y
E	W	L	A	G	Y	I	A	L	Y
F	W	L	T	V	H	L	G	V	Y
G	W	L	A	G	Y	I	A	L	Y
H	W	I	V	G	N	L	F	L	Y
I	W	I	T	A	G	L	S	C	Y
J	W	V	S	C	I	M	G	S	Y
K	F	F	I	T	A	T	G	T	Y
L	W	N	I	S	G	M	L	M	Y
M	W	V	S	S	Y	L	G	L	Y
N	F	T	L	A	L	L	G	S	Y
O	W	N	S	G	P	L	L	M	Y
P	W	N	G	G	I	L	L	I	Y
Q	Y	L	V	T	M	T	G	T	Y
R	W	I	I	S	A	I	L	I	Y
S	W	F	S	S	V	I	L	I	Y
T	W	I	V	A	S	I	F	M	Y
U	W	N	I	S	S	I	L	I	Y
V	L	A	I	G	Q	L	S	I	F
W	S	S	I	A	L	V	G	F	Y
X	L	C	C	G	H	S	L	G	Y
Y	S	F	S	S	V	I	L	V	Y
Z	W	A	S	G	M	L	G	I	Y

Table 9

AA	A	N	L	T	S	T	C	L	Y
BB	L	C	S	A	Y	V	L	L	Y
CC	W	A	T	G	M	L	S	M	Y
DD	M	C	S	S	G	I	L	V	Y
EE	S	G	V	G	L	C	W	F	Y
FF	S	G	A	L	G	V	G	F	Y
GG	S	G	F	A	L	I	G	F	Y
HH	A	G	F	A	L	I	G	F	Y
II	W	V	T	G	L	V	I	S	Y
JJ	W	A	S	G	M	L	G	I	Y
KK	W	I	S	T	Y	L	C	T	Y
LL	W	I	T	T	Y	L	C	T	Y
MM	W	N	I	S	G	M	L	M	Y
NN	A	A	I	G	Q	L	S	I	F
OO	A	I	V	A	S	I	L	I	Y

96. The protein of claim 95, wherein said synthase has 25% or greater sequence identity to SEQ ID NO: 2.

97. The protein of claim 96, wherein said synthase has 35% or greater sequence identity to SEQ ID NO: 2.

98. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a monoterpene substrate.

99. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a sesquiterpene substrate.

100. The synthase of claim 95, wherein said synthase catalyses the formation of a terpenoid product from a diterpene substrate.

101. The synthase of claims 98, 99, or 100, wherein said product is a cyclic terpenoid hydrocarbon.

102. An isolated synthase having a region with 40% or greater sequence identity to residues 343 to 612 of SEQ ID NO: 20, wherein one or more amino acid residues of said synthase that align with amino acids at positions 348, 351, 372, 375, 376, 454, 479, 480, 481, 482, 485, 519, 523, 597, 600, 601, 605, 607 and 608 of SEQ ID NO: 20 are residues other than the following ordered arrangements of residues:

103. An isolated synthase having a region with 40% or greater sequence identity to residues 316 to 586 of SEQ ID NO: 22, wherein one or more amino acid residues of said synthase that align with amino acids at positions 321, 324, 345, 348, 349, 427, 452, 453, 454, 455, 458, 492, 496, 569, 572, 573, 577, 579 and 580 of SEQ ID NO: 22 are residues other than the following ordered arrangements of residues:

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[illegible]

claim 104

[illegible]

105. An isolated synthase having a region with 40% or greater sequence identity to amino acid residues 272 to 540 encoded by SEQ ID NO: 33, wherein one or more amino acid residues of said synthase that align with amino acids at positions 277, 280, 301, 304, 305, 383, 408, 409, 410, 411, 414, 448, 452, 524, 527, 528, 532, 534 and 535 encoded by SEQ ID NO: 33 are residues other than the following ordered arrangements of residues:

09893820-062801

Ordered Arrangement of Residues															
277	A	C	C	W	280	301	304	305	383	409	410	414	448	452	524
278	B	C	G	W	281	302	305	383	409	410	414	448	452	524	527
279	C	G	W	W	282	303	306	384	410	411	415	449	453	525	528
280	D	G	W	W	283	304	307	385	411	412	416	450	454	526	529
281	E	G	W	W	284	305	308	386	412	413	417	451	455	527	530
282	F	G	W	W	285	306	309	387	413	414	418	452	456	528	531
283	G	C	W	W	286	307	310	388	414	415	419	453	457	529	532
284	H	L	P	W	287	308	311	389	415	416	420	454	458	530	533
285	I	K	A	W	288	309	312	390	416	417	421	455	459	531	534
286	J	L	C	W	289	310	313	391	417	418	422	456	460	532	535
287	K	L	C	W	290	311	314	392	418	419	423	457	461	533	536
288	L	C	W	W	291	312	315	393	419	420	424	458	462	534	537
289	M	N	C	W	292	313	316	394	420	421	425	459	463	535	538
290	N	C	W	W	293	314	317	395	421	422	426	460	464	536	539
291	O	C	W	W	294	315	318	396	422	423	427	461	465	537	540
292	P	C	W	W	295	316	319	397	423	424	428	462	466	538	541
293	Q	C	W	W	296	317	320	398	424	425	429	463	467	539	542
294	R	S	C	W	297	318	321	399	425	426	430	464	468	540	543
295	S	S	C	W	298	319	322	400	426	427	431	465	469	541	544
296	T	S	W	W	299	320	323	401	427	428	432	466	470	542	545
297	U	V	W	N	300	321	324	402	428	429	433	467	471	543	546
298	V	V	W	N	301	322	325	403	429	430	434	468	472	544	547
299	W	V	L	S	302	323	326	404	430	431	435	469	473	545	548
300	X	Y	L	S	303	324	327	405	431	432	436	470	474	546	549
301	Y	G	S	C	304	325	328	406	432	433	437	471	475	547	550
302	Z	Y	W	A	305	326	329	407	433	434	438	472	476	548	551
303	AA	A	A	N	306	327	330	408	434	435	439	473	477	549	552
304	BB	C	F	W	307	328	331	409	435	436	440	474	478	550	553
305	CC	F	W	M	308	329	332	410	436	437	441	475	479	551	554
306	DD	V	S	C	309	330	333	411	437	438	442	476	480	552	555
307	EE	V	S	G	310	331	334	412	438	439	443	477	481	553	556
308	FF	C	C	S	311	332	335	413	439	440	444	478	482	554	557
309	GG	C	C	A	312	333	336	414	440	441	445	479	483	555	558
310	HH	C	A	G	313	334	337	415	441	442	446	480	484	556	559
311	II	I	W	W	314	335	338	416	442	443	447	481	485	557	560
312	JJ	I	Y	W	315	336	339	417	443	444	448	482	486	558	561
313	KK	J	Y	W	316	337	340	418	444	445	449	483	487	559	562
314	LL	C	W	W	317	338	341	419	445	446	450	484	488	560	563
315	MM	C	W	W	318	339	342	420	446	447	451	485	489	561	564
316	NN	F	A	A	319	340	343	421	447	448	452	486	490	562	565
317	OO	F	A	A	320	341	344	422	448	449	453	487	491	563	566
318					321	342	345	423	449	450	454	488	492	564	567
319					322	343	346	424	450	451	455	489	493	565	568
320					323	344	347	425	451	452	456	490	494	566	569
321					324	345	348	426	452	453	457	491	495	567	570
322					325	346	349	427	453	454	458	492	496	568	571
323					326	347	350	428	454	455	459	493	497	569	572
324					327	348	351	429	455	456	460	494	498	570	573
325					328	349	352	430	456	457	461	495	499	571	574
326					329	350	353	431	457	458	462	496	500	572	575
327					330	351	354	432	458	459	463	497	501	573	576
328					331	352	355	433	459	460	464	498	502	574	577
329					332	353	356	434	460	461	465	499	503	575	578
330					333	354	357	435	461	462	466	500	504	576	579
331					334	355	358	436	462	463	467	501	505	577	580
332					335	356	359	437	463	464	468	502	506	578	581
333					336	357	360	438	464	465	469	503	507	579	582
334					337	358	361	439	465	466	470	504	508	580	583
335					338	359	362	440	466	467	471	505	509	581	584
336					339	360	363	441	467	468	472	506	510	582	585
337					340	361	364	442	468	469	473	507	511	583	586
338					341	362	365	443	469	470	474	508	512	584	587
339					342	363	366	444	470	471	475	509	513	585	588
340					343	364	367	445	471	472	476	510	514	586	589
341					344	365	368	446	472	473	477	511	515	587	590
342					345	366	369	447	473	474	478	512	516	588	591
343					346	367	370	448	474	475	479	513	517	589	592
344					347	368	371	449	475	476	480	514	518	590	593
345					348	369	372	450	476	477	481	515	519	591	594
346					349	370	373	451	477	478	482	516	520	592	595
347					350	371	374	452	478	479	483	517	521	593	596
348					351	372	375	453	479	480	484	518	522	594	597
349					352	373	376	454	480	481	485	519	523	595	598
350					353	374	377	455	481	482	486	520	524	596	599
351					354	375	378	456	482	483	487	521	525	597	600
352					355	376	379	457	483	484	488	522	526	598	601
353					356	377	380	458	484	485	489	523	527	599	602
354					357	378	381	459	485	486	490	524	528	600	603
355					358	379	382	460	486	487	491	525	529	601	604
356					359	380	383	461	487	488	492	526	530	602	605
357					360	381	384	462	488	489	493	527	531	603	606
358					361	382	385	463	489	490	494	528	532	604	607
359					362	383	386	464	490	491	495	529	533	605	608
360					363	384	387	465	491	492	496	530	534	606	609
361					364	385	388	466	492	493	497	531	535	607	610
362					365	386	389	467	493	494	498	532	536	608	611
363					366	387	390	468	494	495	499	533	537	609	612
364					367	388	391	469	495	496	500	534	538	610	613
365					368	389	392	470	496	497	501	535	539	611	614
366					369	390	393	471	497	498	502	536	540	612	615
367					370	391	394	472	498	499	503	537	541	613	616
368					371	392	395	473	499	500	504	538	542	614	617
369					372	393	396	474	500	501	505	539	543	615	618
370					373	394	397	475	501	502	506	540	544	616	619
371					374	395	398	476	502	503	507	541	545	617	620
372					375	396	399	477	503	504	508	542	546	618	621
373					376	397	400	478	504	505	509	543	547	619	622
374					377	398	401	479	505	506	510	544	548	620	623
375					378	399	402	480	506	507	511	545	549	621	624
376					379	400	403	481	507	508	512	546	550	622	625
377					380	401	404	482	508	509	513	547	5		

106. An isolated synthase having a region with 40% or greater sequence identity to residues 319 to 571 of SEQ ID NO: 42, wherein one or more amino acid residues of said synthase that align with amino acids at positions 324, 327, 348, 351, 352, 430, 455, 456, 457, 458, 461, 495, 499, 571, 574, 575, 579, 581 and 582 of SEQ ID NO: 42 are residues other than the following ordered arrangements of residues:

		Ordered Arrangement of Residues																			
		324	327	348	351	352	430	455	456	457	458	461	465	489	571	574	575	579	581	582	
		A	C	C	G	G	C	C	C	C	C	C	C	C	D	D	D	D	D	D	
B	B	C	G	G	G	G	G	G	G	G	G	G	G	D	D	D	D	D	D	D	
C	C	G	G	G	G	G	G	G	G	G	G	G	G	D	D	D	D	D	D	D	
D	D	G	G	G	G	G	G	G	G	G	G	G	G	D	D	D	D	D	D	D	
E	E	G	G	G	G	G	G	G	G	G	G	G	G	D	D	D	D	D	D	D	
F	F	G	G	G	G	G	G	G	G	G	G	G	G	D	D	D	D	D	D	D	
G	G	C	C	C	C	C	C	C	C	C	C	C	C	D	D	D	D	D	D	D	
H	H	C	C	C	C	C	C	C	C	C	C	C	C	D	D	D	D	D	D	D	
I	I	P	A	W	V	D	G	F	A	G	N	L	S	S	O	O	O	O	O	O	
J	J	A	W	F	V	C	G	A	E	I	S	A	G	N	P	P	P	P	P	P	
K	K	N	F	F	L	I	T	V	S	S	S	T	L	G	Q	Q	Q	Q	Q	Q	
L	L	C	W	N	V	L	V	V	S	S	S	T	L	G	R	R	R	R	R	R	
M	M	N	W	F	L	L	V	N	A	T	L	L	L	L	S	S	S	S	S	S	
N	N	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
O	O	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
P	P	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
Q	Q	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
R	R	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
S	S	C	W	N	V	T	V	V	I	S	G	L	L	L	T	T	T	T	T	T	
T	T	S	W	I	A	T	V	S	S	V	A	S	I	L	N	N	N	N	N	N	
U	U	N	W	N	A	L	T	V	S	S	S	I	L	N	N	N	N	N	N	N	
V	V	F	I	A	Q	T	V	V	S	I	S	L	L	N	N	N	N	N	N	N	
W	W	I	L	S	T	T	V	V	S	I	A	L	L	N	N	N	N	N	N	N	
X	X	I	L	S	T	T	V	V	S	I	A	L	L	N	N	N	N	N	N	N	
Y	Y	G	S	C	F	I	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
Z	Z	Y	W	A	C	L	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
AA	AA	F	L	M	C	V	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
BB	BB	F	L	M	C	V	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
CC	CC	F	L	M	C	V	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
DD	DD	V	S	S	G	Q	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
EE	EE	C	S	S	G	Q	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
FF	FF	C	S	S	G	Q	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
GG	GG	C	S	S	G	Q	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
HH	HH	C	S	S	G	Q	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
II	II	I	W	V	A	C	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
JJ	JJ	I	W	V	A	C	T	V	S	S	S	L	L	N	N	N	N	N	N	N	
KK	KK	C	W	I	I	S	V	T	T	T	T	L	L	N	N	N	N	N	N	N	
LL	LL	C	W	I	I	S	V	T	T	T	T	L	L	N	N	N	N	N	N	N	
MM	MM	C	W	I	I	S	V	T	T	T	T	L	L	N	N	N	N	N	N	N	
NN	NN	C	W	I	I	S	V	T	T	T	T	L	L	N	N	N	N	N	N	N	
OO	OO	F	A	A	A	T	V	S	S	V	A	S	I	L	N	N	N	N	N	N	

107. An isolated synthase having a region with 40% or greater sequence identity to residues 579 to 847 of SEQ ID NO: 44, wherein one or more amino acid residues of said synthase that align with amino acids at positions 584, 587, 606, 609, 610, 688, 713, 714, 715, 716, 719, 753, 757, 831, 834, 835, 839, 841 and 842 of SEQ ID NO: 44 are residues other than the following ordered arrangements of residues:

Ordered Arrangement of Residues															
584	597	606	609	610	698	713	714	715	716	753	831	834	835	839	841
A	C	W	I	I	S	Y	T	T	Y	L	V	T	Y	D	Y
B	C	G	I	I	S	Y	T	T	Y	L	V	T	Y	D	Y
C	G	W	I	I	S	Y	T	T	Y	L	V	T	Y	D	Y
D	C	G	W	I	S	Y	T	T	Y	L	V	T	Y	D	Y
E	G	W	L	L	S	Y	T	T	Y	L	V	T	Y	D	Y
F	G	W	L	L	S	Y	T	T	Y	L	V	T	Y	D	Y
G	C	W	L	L	S	Y	T	T	Y	L	V	T	Y	D	Y
H	C	W	L	L	S	Y	T	T	Y	L	V	T	Y	D	Y
I	P	A	I	V	D	E	T	T	A	G	C	S	Y	D	Y
J	K	A	F	V	C	G	A	E	T	A	G	C	S	Y	D
K	N	F	N	I	T	Y	S	I	S	G	N	C	Y	D	Y
L	C	W	N	V	L	T	Y	S	T	L	A	M	Y	D	Y
M	N	F	N	V	L	T	Y	S	T	L	A	M	Y	D	Y
N	C	W	N	V	L	T	Y	S	T	L	A	M	Y	D	Y
O	C	W	N	V	L	T	Y	S	T	L	A	M	Y	D	Y
P	C	Y	L	V	T	F	A	G	T	D	A	T	Y	D	Y
Q	C	Y	L	V	T	F	A	G	T	D	A	T	Y	D	Y
R	S	S	W	I	I	Y	F	S	I	L	N	A	Y	D	Y
S	S	S	W	I	I	Y	F	S	I	L	N	A	Y	D	Y
T	U	N	W	A	T	Y	S	S	I	L	N	A	Y	D	Y
U	N	W	A	T	Y	S	S	S	I	L	N	A	Y	D	Y
V	F	L	S	A	Q	T	Y	S	I	L	N	A	Y	D	Y
W	I	S	L	S	C	T	Y	S	I	L	N	A	Y	D	Y
X	Y	L	C	F	I	T	F	S	S	L	N	A	Y	D	Y
Y	G	S	C	I	T	F	S	S	S	L	N	A	Y	D	Y
Z	Y	W	A	C	T	Y	N	S	S	L	N	A	Y	D	Y
AA	A	A	N	A	L	T	Y	A	S	L	N	A	Y	D	Y
BB	F	L	C	A	M	T	Y	S	T	L	N	A	Y	D	Y
CC	F	L	C	A	M	T	Y	S	T	L	N	A	Y	D	Y
DD	V	M	C	Q	T	Y	N	S	S	L	N	A	Y	D	Y
EE	V	S	G	Q	T	Y	N	S	S	L	N	A	Y	D	Y
FF	C	S	G	T	T	M	S	F	A	L	L	V	Y	D	Y
GG	C	S	G	T	T	M	S	F	A	L	L	V	Y	D	Y
HH	C	S	G	T	T	M	S	F	A	L	L	V	Y	D	Y
II	I	W	A	C	I	S	Y	T	T	L	N	A	Y	D	Y
JJ	C	W	A	C	I	S	Y	T	T	L	N	A	Y	D	Y
KK	C	W	A	C	I	S	Y	T	T	L	N	A	Y	D	Y
LL	C	W	A	C	I	S	Y	T	T	L	N	A	Y	D	Y
MM	C	W	A	C	I	S	Y	T	T	L	N	A	Y	D	Y
NN	F	A	A	Q	T	Y	S	I	S	G	Q	L	Y	D	Y
OO	F	A	A	Q	T	Y	S	I	S	G	Q	L	Y	D	Y

108. An isolated synthase having a region with 40% or greater sequence identity to residues 495 to 767 of SEQ ID NO: 46, wherein one or more amino acid residues of said synthase that align with amino acids at positions 500, 503, 524, 527, 528, 606, 631, 632, 633, 634, 637, 674, 678, 751, 754, 755, 759, 761 and 762 of SEQ ID NO: 46 are residues other than the following ordered arrangements of residues:

109. An isolated synthase having a region with 40% or greater sequence identity to residues 295 to 564 of SEQ ID NO: 48, wherein one or more amino acid residues of said synthase that align with amino acids at positions 300, 303, 324, 327, 328, 406, 431, 432, 433, 434, 437, 471, 475, 548, 551, 552, 556, 558 and 559 of SEQ ID NO: 48 are residues other than the following ordered arrangements of residues:

08897620-067801
108290-0286689

108290-02836360

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Ordered Arrangement of Residues															
300	303	324	327	328	408	431	432	433	434	437	471	475	548	551	552
A	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
B	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
C	G	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
D	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
E	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
F	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
G	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
H	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
I	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
J	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
K	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
L	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
M	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
N	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
O	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
P	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
Q	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
R	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
S	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
T	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
U	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
V	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
W	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
X	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
Y	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
Z	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
AA	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
BB	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
CC	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
DD	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
EE	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
FF	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
GG	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
HH	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
II	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
JJ	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
KK	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
LL	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
MM	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
NN	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V
OO	C	W	L	S	Y	S	T	G	H	L	G	N	A	L	V

110. An isolated synthase having a region with 40% or greater sequence identity to residues 307 to 578 of SEQ ID NO: 50, wherein one or more amino acid residues of said synthase that align with amino acids at positions 312, 315, 336, 339, 340, 419, 444, 445, 446, 447, 450, 484, 488, 562, 565, 566, 570, 572 and 573 of SEQ ID NO: 50 are residues other than the following ordered arrangements of residues:

108290.0286866

Ordered Arrangement of Residues															
312	315	338	339	340	419	444	445	446	447	450	484	562	565	566	570
A	C	W	I	I	S	Y	T	S	T	Y	L	V	T	Y	D
B	C	W	I	I	S	Y	T	S	T	Y	L	C	L	Y	D
C	G	W	I	A	S	Y	T	C	G	Y	L	M	L	Y	D
D	G	W	L	A	S	Y	S	A	G	Y	L	A	L	Y	D
E	C	W	L	L	S	Y	S	A	V	H	L	A	L	Y	D
F	C	W	L	L	S	Y	S	A	G	N	L	A	L	Y	D
G	C	W	L	L	S	Y	S	A	V	G	L	A	L	Y	D
H	P	W	I	T	D	Y	S	T	A	G	L	V	C	Y	D
I	A	W	V	C	G	F	E	I	T	A	M	C	S	Y	D
J	A	F	L	I	T	V	S	I	S	G	N	A	S	Y	D
K	N	W	F	L	T	V	S	I	S	G	N	A	L	Y	D
L	S	W	N	L	T	V	S	I	S	G	N	A	L	Y	D
M	N	F	N	L	T	V	S	I	S	G	N	A	L	Y	D
N	C	W	N	V	T	V	I	S	G	L	L	A	M	Y	D
P	C	W	L	V	T	F	A	I	G	L	L	A	I	Y	D
Q	C	W	L	V	T	F	A	I	G	L	L	A	I	Y	D
R	C	W	L	V	T	F	A	I	S	V	L	A	I	Y	D
S	W	F	I	T	V	S	I	S	S	V	L	A	I	Y	D
T	S	W	N	A	T	V	S	I	S	S	L	A	M	Y	D
U	V	F	L	T	V	S	I	S	S	S	L	A	M	Y	D
V	F	L	S	A	T	V	S	I	S	S	L	A	M	Y	D
W	Y	L	S	T	V	S	I	S	S	S	L	A	M	Y	D
X	Y	L	S	T	V	S	I	S	S	S	L	A	M	Y	D
Y	G	S	C	I	T	F	S	C	G	H	V	L	F	Y	D
Z	Y	W	A	C	T	V	S	S	S	S	L	A	V	Y	D
AA	A	A	N	L	T	V	S	S	S	S	L	A	V	Y	D
BB	F	A	C	A	T	V	S	S	S	S	L	A	V	Y	D
CC	F	L	C	M	T	V	S	S	S	S	L	A	V	Y	D
DD	V	M	C	V	T	F	S	S	S	S	L	A	V	Y	D
EE	V	M	C	V	T	F	S	S	S	S	L	A	V	Y	D
FF	V	M	C	V	T	F	S	S	S	S	L	A	V	Y	D
GG	C	S	G	T	T	M	F	A	L	L	I	L	F	Y	D
HH	C	S	G	T	T	M	F	A	L	L	I	L	F	Y	D
II	C	A	G	T	T	M	F	A	L	L	I	L	F	Y	D
JJ	Y	W	A	C	T	V	S	S	S	S	L	A	V	Y	D
KK	Y	W	A	C	T	V	S	S	S	S	L	A	V	Y	D
LL	C	W	I	I	S	Y	T	T	Y	G	L	C	D	Y	D
MM	C	W	I	I	S	Y	T	T	Y	G	L	C	D	Y	D
NN	F	A	A	Q	T	Y	S	I	S	Q	L	S	D	F	D
OO	F	A	A	Q	T	Y	S	I	S	Q	L	S	D	F	D

111. An isolated synthase having a region with 40% or greater sequence identity to residues 264 to 533 of SEQ ID NO: 52, wherein one or more amino acid residues of said synthase that align with amino acids at positions 269, 272, 293, 296, 297, 375, 401, 402, 403, 404, 407, 441, 445, 517, 520, 521, 525, 527 and 528 of SEQ ID NO: 52 are residues other than the following ordered arrangements of residues:

03037022-062904
108290-02838930

112. An isolated synthase having a region with 40% or greater sequence identity to residues 585 to 853 of SEQ ID NO: 56, wherein one or more amino acid residues of said synthase that align with amino acids at positions 590, 593, 614, 617, 618, 696, 721, 722, 723, 724, 727, 761, 765, 837, 840, 841, 845, 847 and 848 of SEQ ID NO: 56 are residues other than the following ordered arrangements of residues:

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113. An isolated synthase having a region with 40% or greater sequence identity to residues 307 to 574 of SEQ ID NO: 54, wherein one or more amino acid residues of said synthase that align with amino acids at positions 312, 315, 336, 339, 340, 418, 443, 444, 445, 446, 449, 483, 487, 560, 563, 564, 566, 568 and 569 of SEQ ID NO: 54 are residues other than the following ordered arrangements of residues:

108290-0236890

Ordered Arrangement of Residues															
312	315	336	339	340	418	443	444	445	446	449	463	487	500	563	564
A	C	W	I	S	Y	T	T	T	T	L	C	D	V	I	Y
B	C	W	I	S	Y	T	S	G	Y	L	C	D	M	L	Y
C	G	W	I	S	Y	T	S	G	Y	L	C	D	M	L	Y
D	G	W	I	S	Y	T	S	G	Y	L	C	D	M	L	Y
E	G	W	L	S	Y	S	I	A	G	H	I	G	N	A	Y
F	G	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
G	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
H	L	P	I	D	Y	S	I	A	G	N	L	F	A	V	Y
I	A	W	V	G	F	E	I	S	C	I	A	G	N	A	Y
J	K	N	L	S	Y	S	I	A	G	N	L	F	A	V	Y
K	A	W	V	G	F	E	I	S	C	I	A	G	N	A	Y
L	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
M	N	C	V	N	Y	A	S	G	L	P	L	G	N	A	Y
N	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
O	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
P	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
Q	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
R	C	W	L	S	Y	S	I	A	G	N	L	F	A	V	Y
S	S	W	F	I	V	E	S	S	A	S	I	L	N	A	Y
T	S	W	F	I	V	E	S	S	A	S	I	L	N	A	Y
U	V	N	A	T	Y	S	I	S	Q	L	V	S	D	N	Y
V	F	L	S	C	Y	S	I	S	Q	L	V	S	D	N	Y
W	L	S	C	Y	S	I	S	Q	L	V	S	D	N	Y	Y
X	L	S	C	Y	S	I	S	Q	L	V	S	D	N	Y	Y
Y	G	F	I	T	Y	S	I	S	Q	L	V	S	D	N	Y
Z	Y	W	A	T	Y	S	I	S	Q	L	V	S	D	N	Y
AA	A	N	C	L	Y	S	I	S	Q	L	V	S	D	N	Y
BB	F	A	C	W	T	Y	S	S	G	M	T	L	N	A	Y
CC	F	W	M	T	Y	S	S	G	M	T	L	N	A	Y	Y
DD	V	M	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
EE	S	G	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
FF	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
GG	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
HH	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
II	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
JJ	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
KK	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
LL	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
MM	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
NN	C	S	G	V	Y	S	S	G	M	T	L	N	A	Y	Y
OO	F	A	I	T	Y	S	I	S	Q	L	V	S	D	N	Y

114. An isolated synthase having a region with 40% or greater sequence identity to residues 309 to 577 of SEQ ID NO: 24, wherein one or more amino acid residues of said synthase that align with amino acids at positions 314, 317, 338, 341, 342, 420, 446, 447, 448, 449, 452, 485, 489, 560, 563, 564, 569, 571 and 572 of SEQ ID NO: 24 are residues other than the following ordered arrangements of residues:

103290.02868650

Ordered Arrangement of Residues															
314	317	318	341	342	420	446	447	448	449	452	485	560	563	564	569
A	C	C	I	I	S	T	T	T	T	L	C	D	T	Y	D
B	C	C	I	S	Y	G	C	G	Y	L	C	D	I	Y	D
C	G	G	A	S	Y	T	S	G	Y	L	C	D	L	Y	D
D	G	G	A	S	Y	S	A	G	Y	L	C	D	L	Y	D
E	C	C	L	S	Y	S	I	G	N	L	A	D	V	Y	D
F	C	C	L	S	Y	S	A	G	N	L	A	D	V	Y	D
G	L	W	I	T	Y	S	Y	A	C	L	S	D	A	Y	D
H	L	W	I	T	Y	S	Y	A	C	L	S	D	A	Y	D
I	A	F	V	G	E	I	S	S	T	A	G	N	I	Y	D
K	A	F	L	G	Y	I	S	S	T	A	G	N	I	Y	D
L	C	N	I	T	Y	S	S	S	A	L	L	G	V	Y	D
M	N	F	L	T	Y	N	A	G	A	L	L	G	V	Y	D
N	N	F	L	T	Y	N	A	G	A	L	L	G	V	Y	D
O	C	W	N	T	Y	Y	I	G	I	L	L	D	A	Y	D
P	C	W	N	T	Y	Y	I	G	I	L	L	D	A	Y	D
R	C	W	N	T	Y	Y	I	G	I	L	L	D	A	Y	D
S	W	F	I	T	Y	F	S	S	Y	I	L	D	A	Y	D
T	W	N	L	T	Y	F	S	S	Y	I	L	D	A	Y	D
V	W	N	L	T	Y	F	S	S	Y	I	L	D	A	Y	D
W	Y	I	C	T	Y	S	I	G	A	L	L	G	V	Y	D
X	Y	S	I	T	Y	S	I	G	A	L	L	G	V	Y	D
Y	G	F	I	T	Y	S	S	S	S	S	L	G	V	Y	D
Z	W	A	C	T	Y	N	S	A	L	T	C	L	L	Y	D
AA	A	A	L	C	T	N	S	A	L	T	C	L	L	Y	D
BB	F	A	C	T	Y	N	S	A	L	T	C	L	L	Y	D
CC	F	W	C	M	Y	N	S	A	L	T	C	L	L	Y	D
DD	Y	S	G	Q	Y	V	S	G	L	C	W	N	L	Y	D
EE	V	S	G	Q	Y	V	S	G	L	C	W	N	L	Y	D
FF	C	S	G	T	Y	M	S	F	A	L	L	G	V	Y	D
GG	C	S	G	T	Y	M	S	F	A	L	L	G	V	Y	D
HH	C	A	G	T	Y	M	S	F	A	L	L	G	V	Y	D
II	Y	W	V	I	S	Y	T	S	T	Y	G	L	V	Y	D
JJ	Y	W	V	I	S	Y	T	S	T	Y	G	L	V	Y	D
KK	C	W	I	I	S	Y	T	S	T	Y	G	L	V	Y	D
LL	C	W	I	I	S	Y	T	S	T	Y	G	L	V	Y	D
MM	C	W	I	I	S	Y	T	S	T	Y	G	L	V	Y	D
NN	F	A	Q	A	S	I	S	G	O	S	L	D	A	Y	D
OO	F	A	Q	A	S	I	S	G	O	S	L	D	A	Y	D

115. An isolated synthase having a region with 40% or greater sequence identity to residues 315 to 584 of SEQ ID NO: 26, wherein one or more amino acid residues of said synthase that align with amino acids at positions 320, 323, 344, 347, 348, 426, 451, 452, 453, 454, 457, 492, 496, 568, 571, 572, 576, 578 and 579 of SEQ ID NO: 26 are residues other than the following ordered arrangements of residues:

03833820-062804
108290-02855860

116. An isolated synthase having a region with 40% or greater sequence identity to residues 265 to 536 of SEQ ID NO: 28, wherein one or more amino acid residues of said synthase that align with amino acids at positions 270, 273, 294, 297, 298, 376, 401, 402, 403, 404, 407, 440, 444, 518, 521, 522, 528, 530 and 531 of SEQ ID NO: 28 are residues other than the following ordered arrangements of residues:

117. An isolated synthase having a region with 40% or greater sequence identity to residues 342 to 612 of SEQ ID NO: 30, wherein one or more amino acid residues of said synthase that align with amino acids at positions 347, 350, 371, 374, 375, 453, 478, 479, 480, 481, 483, 518, 522, 596, 599, 600, 604, 606 and 607 of SEQ ID NO: 30 are residues other than the following ordered arrangements of residues:

108230-0233390

Ordered Arrangement of Residues															
347	350	371	374	375	453	478	479	480	481	483	518	522	596	599	600
604	606	607													
A	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
B	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
C	C	W	I	S	Y	T	T	T	Y	L	C	D	V	T	Y
D	G	W	L	S	Y	S	A	G	Y	L	C	N	A	L	Y
E	C	W	L	S	Y	S	A	G	Y	L	C	N	A	L	Y
F	C	W	L	S	Y	S	A	G	Y	L	C	N	A	L	Y
G	C	W	L	S	Y	S	A	G	Y	L	C	N	A	L	Y
H	L	W	I	T	Y	S	V	A	G	N	L	F	A	C	Y
I	P	W	I	V	D	Y	S	T	C	I	M	G	A	S	Y
J	A	W	F	C	G	A	E	I	T	A	G	N	A	S	Y
K	N	F	L	T	Y	S	S	I	S	G	M	L	A	T	Y
L	C	W	N	V	N	A	S	S	Y	L	G	N	L	M	Y
M	S	W	L	T	Y	S	S	I	S	G	M	L	A	T	Y
N	N	F	L	T	Y	S	S	I	S	G	M	L	A	T	Y
O	C	W	N	V	N	A	S	S	Y	L	G	N	L	M	Y
P	C	W	L	T	Y	S	S	I	S	G	M	L	A	T	Y
Q	C	W	L	T	Y	S	S	I	S	G	M	L	A	T	Y
R	C	W	L	T	Y	S	S	I	S	G	M	L	A	T	Y
S	S	W	F	I	V	F	S	S	S	V	I	L	N	A	Y
T	S	W	N	L	T	Y	S	S	I	S	G	M	L	A	Y
U	N	W	N	L	T	Y	S	S	I	S	G	M	L	A	Y
V	F	L	A	T	Y	S	S	I	S	G	M	L	A	T	Y
W	I	S	T	Y	S	S	C	G	H	V	I	L	N	A	Y
X	Y	L	C	T	Y	S	S	S	S	G	M	L	A	T	Y
Y	G	S	I	T	Y	S	S	S	S	G	M	L	A	T	Y
Z	Y	A	C	T	Y	S	S	S	S	G	M	L	A	T	Y
AA	F	A	N	L	T	Y	S	S	S	T	C	M	L	L	Y
BB	F	A	N	L	T	Y	S	S	S	T	C	M	L	L	Y
CC	F	W	A	C	V	T	Y	S	S	A	G	M	L	L	Y
DD	F	W	A	C	V	T	Y	S	S	A	G	M	L	L	Y
EE	V	S	C	Q	V	V	S	S	S	L	G	N	L	M	Y
FF	C	S	G	T	T	M	S	F	A	L	L	G	N	L	Y
GG	C	S	G	T	T	M	S	F	A	L	L	G	N	L	Y
HH	C	S	G	T	T	M	S	F	A	L	L	G	N	L	Y
II	I	W	A	S	Y	T	S	T	G	L	V	I	G	N	Y
JJ	Y	W	A	S	Y	T	S	T	G	L	V	I	G	N	Y
KK	Y	W	A	S	Y	T	S	T	G	L	V	I	G	N	Y
LL	C	W	I	S	Y	T	S	T	G	L	V	I	G	N	Y
MM	C	W	I	S	Y	T	S	T	G	L	V	I	G	N	Y
NN	F	A	A	Q	T	Y	S	I	G	Q	S	D	A	T	Y
OO	F	A	A	Q	T	Y	S	I	G	Q	S	D	A	T	Y

118. An isolated synthase having a region with about 40% or greater sequence identity to residues 307 to 541 of SEQ ID NO: 32, wherein one or more amino acid residues of said synthase that align with amino acids at positions 278, 281, 302, 305, 306, 384, 409, 410, 411, 412, 415, 448, 452, 524, 527, 528, 533, 535 and 536 of SEQ ID NO: 32 are residues other than the following ordered arrangements of residues:

100290-020200

		Ordered Arrangement of Residues																		
		278	281	302	305	306	384	409	410	411	412	415	448	452	504	527	528	533	535	536
A	C	C	W	I	I	S	Y	T	T	T	Y	L	C	D	D	I	Y	D	Y	T
B	C	W	I	I	S	Y	Y	T	T	S	G	Y	L	C	D	I	T	Y	D	T
C	G	W	I	A	S	Y	T	T	C	G	Y	L	C	D	M	L	L	Y	D	T
D	C	W	L	T	S	Y	S	A	T	G	Y	L	A	D	A	L	L	Y	D	T
E	C	W	L	T	S	Y	S	A	T	G	Y	L	A	D	A	L	L	Y	D	T
F	G	W	L	T	S	Y	S	A	T	G	Y	L	A	D	A	L	L	Y	D	T
G	C	W	L	T	S	Y	S	A	T	G	Y	L	A	D	A	L	L	Y	D	T
H	L	P	W	I	V	D	E	T	A	C	G	N	L	S	D	A	C	Y	D	T
I	P	W	I	V	C	G	E	T	A	C	G	N	L	S	D	A	C	Y	D	T
J	K	N	F	L	I	T	Y	S	I	S	Y	L	M	G	N	I	Y	E	F	T
K	N	F	L	I	T	Y	S	I	S	Y	L	M	G	N	I	Y	E	F	T	T
L	N	S	F	L	L	T	Y	S	I	S	Y	L	M	G	N	I	Y	E	F	T
M	N	S	F	L	L	T	Y	S	I	S	Y	L	M	G	N	I	Y	E	F	T
N	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
O	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
P	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
Q	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
R	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
S	C	W	N	V	L	T	Y	I	G	T	P	L	L	L	D	A	I	Y	D	T
T	S	W	N	C	T	Y	S	I	S	S	A	S	I	F	N	S	I	Y	D	T
U	N	L	S	C	T	Y	S	I	S	S	A	S	I	F	N	S	I	Y	D	T
V	N	L	S	C	T	Y	S	I	S	S	A	S	I	F	N	S	I	Y	D	T
W	X	G	S	L	I	T	Y	S	C	G	H	V	I	L	N	A	V	Y	D	T
X	G	S	L	I	T	Y	S	C	G	H	V	I	L	N	A	V	Y	D	T	S
Y	S	L	I	T	Y	S	C	G	H	V	I	L	N	A	V	Y	D	T	S	S
Z	A	W	A	N	L	T	Y	N	A	S	L	T	S	G	M	L	L	Y	D	T
AA	A	L	C	V	T	Y	N	A	S	L	T	S	G	M	L	L	Y	D	T	S
BB	E	L	C	V	T	Y	N	A	S	L	T	S	G	M	L	L	Y	D	T	S
CC	E	L	C	V	T	Y	N	A	S	L	T	S	G	M	L	L	Y	D	T	S
DD	V	S	G	O	T	Y	V	S	G	L	C	W	N	L	F	Y	D	F	T	T
EE	V	S	G	O	T	Y	V	S	G	L	C	W	N	L	F	Y	D	F	T	T
FF	C	S	G	T	T	T	M	S	F	A	L	L	I	G	N	T	S	Y	D	T
GG	C	S	G	T	T	T	M	S	F	A	L	L	I	G	N	T	S	Y	D	T
HH	C	A	V	I	S	Y	T	S	T	G	M	L	L	C	D	L	I	Y	D	T
II	V	W	I	C	T	Y	Y	T	T	G	M	L	L	C	D	L	I	Y	D	T
JJ	V	W	I	C	T	Y	Y	T	T	G	M	L	L	C	D	L	I	Y	D	T
KK	C	W	N	I	I	S	Y	T	T	S	G	M	L	L	C	D	I	M	F	T
LL	C	W	N	I	I	S	Y	T	T	S	G	M	L	L	C	D	I	M	F	T
MM	C	W	N	I	I	S	Y	T	T	S	G	M	L	L	C	D	I	M	F	T
NN	F	A	A	Q	A	T	Y	S	I	S	G	Q	L	L	D	A	I	Y	D	T
OO	F	A	A	Q	A	T	Y	S	I	S	G	Q	L	L	D	A	I	Y	D	T

119.

A method for making a terpene synthase, comprising:

- a) identifying, in a preselected polypeptide having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, nine amino acid residues whose α -carbons have interatomic distances in Angstroms between said α -carbons that are ± 2.3 Angstroms of the following interatomic distances:

α -Carbon	1	2	3	4	5	6	7	8	9
1	0.0	8.4	13.7	12.7	11.9	10.2	13.1	9.4	12.8
2	8.4	0.0	11.3	8.7	10.2	7.2	14.8	15.1	17.4
3	13.7	11.3	0.0	3.8	5.4	9.3	6.6	13.9	13.7
4	12.7	8.7	3.8	0.0	3.8	6.0	9.2	15.4	16.1
5	11.9	10.2	5.4	3.8	0.0	5.0	7.8	14.6	15.5
6	10.2	7.2	9.3	6.0	5.0	0.0	12.0	16.1	18.0
7	13.1	14.8	6.6	9.2	7.8	12.0	0.0	10.2	9.5
8	9.4	15.1	13.9	15.4	14.6	16.1	10.2	0.0	3.8
9	12.8	17.4	13.7	16.1	15.5	18.0	9.5	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	120.203	38.695	43.506
2	114.058	43.884	41.015
3	106.807	36.336	45.151
4	107.629	38.010	41.804
5	109.375	34.842	40.617
6	111.944	37.854	37.602
7	110.233	31.098	47.361
8	118.846	34.443	51.796
9	116.461	32.848	54.290

; and

- b) synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having one or more R-groups associated with said α -carbons other than the R-groups associated with said α -carbons in said preselected polypeptide, wherein said modified polypeptide has terpene synthase activity.

120. The method of claim 119, wherein said synthesizing step comprises the formation of a nucleic acid encoding said preselected polypeptide in which the coding sequence for one or more amino acids corresponding to said nine α -carbons is replaced by a coding sequence that codes for an amino acid different from the amino acid present in said preselected polypeptide.

121. The method of claim 119, wherein said preselected polypeptide is a pinene synthase.

122. The method of claim 121, wherein said preselected polypeptide is SEQ ID NO: 20.

123. The method of claim 119, wherein said preselected polypeptide is a taxadiene synthase.

124. The method of claim 123, wherein said preselected polypeptide is SEQ ID NO: 44.

125. A method of using a terpene synthase, comprising:

a) identifying, in a preselected polypeptide having a region with 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, amino acid residues at nine positions that align with amino acid residues at positions 273, 294, 402, 403, 404, 407, 440, 519 and 520 of SEQ ID NO: 2; and

b) synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having amino acid residues at one or more of said nine positions other than the amino acid residues present in said preselected polypeptide.

126. The method of claim 125, wherein said identifying step comprises identifying sixteen amino acid residues in said preselected polypeptide that align with amino acid residues at positions 270, 273, 294, 297, 298, 402, 403, 404, 407, 440, 516, 519, 520, 525, 527 and 528 of SEQ ID NO: 2, and said synthesizing step comprises synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having amino acid residues at one or more of said sixteen positions other than the amino acid residues present in said preselected polypeptide.

127. The method of claim 125, wherein said identifying step comprises identifying nineteen amino acid residues in said preselected polypeptide that align with amino acid residues at positions 270, 273, 294, 297, 298, 376, 401, 402, 403, 404, 407, 440, 444, 516, 519, 520, 525, 527 and 528 of SEQ ID NO: 2, and said synthesizing step comprises synthesizing a polypeptide that is modified from said preselected polypeptide, said modified polypeptide having amino acid residues at one or more of said nineteen positions other than the amino acid residues present in said preselected polypeptide.

128. The method of claim 125, wherein said synthesizing step comprises the formation of a nucleic acid encoding said preselected polypeptide in which the coding sequence in said nucleic acid coding for one or more of said nine amino acid residues is replaced by a coding sequence that codes for an amino acid different from the amino acid present in said preselected polypeptide.

129. The method of claim 125, wherein said preselected polypeptide is a pinene synthase.

130. The method of claim 129, wherein said preselected polypeptide is SEQ ID
NO: 20.

131. The method of claim 125, wherein said preselected polypeptide is a taxadiene synthase.

132. The method of claim 131, wherein said preselected polypeptide is SEQ ID
NO: 44.

133. The method of claim 125, further comprising:

- c) contacting said modified polypeptide with an isoprenoid substrate under conditions effective for said substrate to bind said synthase; and
- d) measuring the ability of said modified polypeptide to catalyze the formation of a reaction product from said substrate.

134. The method of claim 133, wherein said isoprenoid substrate is a geranyl diphosphate.

135. The method of claim 133, wherein said isoprenoid substrate is a farnesyl diphosphate.

136. The method of claim 133, wherein said isoprenoid substrate is a geranyl genanylyl diphosphate.

137. A method of making a terpene synthase, comprising:
creating a population of nucleic acid molecules that encode polypeptides, said population having members that differ from one another at one or more of nine codons specifying amino acids in a region of a preselected terpene synthase polypeptide having 20% or greater sequence identity to residues 265 to 535 of SEQ ID NO: 2, α -carbons of said nine amino acids having interatomic distances in Angstroms between said α -carbons that are ± 2.3 Angstroms of the following interatomic distances:

α -Carbon	1	2	3	4	5	6	7	8	9
1	0.0	8.4	13.7	12.7	11.9	10.2	13.1	9.4	12.8
2	8.4	0.0	11.3	8.7	10.2	7.2	14.8	15.1	17.4
3	13.7	11.3	0.0	3.8	5.4	9.3	6.6	13.9	13.7
4	12.7	8.7	3.8	0.0	3.8	6.0	9.2	15.4	16.1
5	11.9	10.2	5.4	3.8	0.0	5.0	7.8	14.6	15.5
6	10.2	7.2	9.3	6.0	5.0	0.0	12.0	16.1	18.0
7	13.1	14.8	6.6	9.2	7.8	12.0	0.0	10.2	9.5
8	9.4	15.1	13.9	15.4	14.6	16.1	10.2	0.0	3.8
9	12.8	17.4	13.7	16.1	15.5	18.0	9.5	3.8	0.0

the center point of each said α -carbon positioned within a sphere having a radius of 2.3 Angstroms, the center point of each said sphere having the following structural coordinates:

α -Carbon Number	X Position	Y Position	Z Position
1	120.203	38.695	43.506
2	114.058	43.884	41.015
3	106.807	36.336	45.151
4	107.629	38.010	41.804
5	109.375	34.842	40.617
6	111.944	37.854	37.602
7	110.233	31.098	47.361
8	118.846	34.443	51.796
9	116.461	32.848	54.290

; and

b) expressing at least a portion of said nucleic acid population so that a population of polypeptides is made, wherein at least one member of said population of polypeptides is a mutant terpene synthase.

138. The method of claim 137, wherein said expressing step comprises *in vitro* transcription and *in vitro* translation of said nucleic acid populations.

139. The method of claim 137, wherein said expressing step comprises:

- i) cloning said members of said nucleic acid population into an expression vector;
- ii) introducing, into host cells, said cloned nucleic acid population members in said expression vector; and
- iii) expressing said cloned nucleic acid population members in said host cells so that said population of polypeptides is made.

140. The method of claim 139, wherein said host cells are prokaryotic cells.

141. The method of claim 137, wherein said preselected terpene synthase polypeptide is a monoterpene synthase.

142. The method of claim 137, wherein said preselected terpene synthase polypeptide is a sesquiterpene synthase.

143. The method of claim 137, wherein said preselected terpene synthase polypeptide is a diterpene synthase.
144. An isolated nucleic acid encoding the synthase of claim 1.
145. An isolated nucleic acid encoding the synthase of claim 2.
146. An isolated nucleic acid encoding the synthase of claim 3.
147. An isolated nucleic acid encoding the synthase of claim 7.
148. An isolated nucleic acid encoding a synthase selected from the group consisting of the synthase of claims 11 through 73.
149. An isolated nucleic acid encoding the synthase of claim 80.
150. An isolated nucleic acid encoding the synthase of claim 88.
151. An isolated nucleic acid encoding the synthase of claim 95.
152. An isolated nucleic acid encoding a synthase selected from the group consisting of the synthase of claims 102 through 118.
153. A host cell containing a nucleic acid encoding the synthase of claim 1.
154. The host cell of claim 153, wherein said cell is a prokaryotic cell.
155. The host cell of claim 153, wherein said cell is a eukaryotic cell.
156. The host cell of claim 155, wherein said cell is an insect cell.
157. The host cell of claim 155, wherein said cell is a plant cell.
158. The host cell of claim 157, wherein said host cell is an Angiosperm cell.

159. The host cell of claim 157, wherein said host cell is an Gymnosperm cell.

160. The host cell of claim 157, wherein said host cell is selected from the group consisting of: a cell from a Graminaceae plant, a cell from a Legumineae plant, a cell from a Solanaceae plant, a cell from a Brassicaceae plant and a cell from a Conifereae plant.

161. A transgenic plant containing a nucleic acid encoding the synthase of claim 1.

162. A transgenic animal cell culture containing a nucleic acid encoding the synthase of claim 1.